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RAW SEQUENCE LISTING
PATENT APPLICATION: US/10/047,991

DATE: 05/28/2002
TIME: 09:24:23

Input Set : A:\Hmv08001.app
Output Set: N:\CRF3\05282002\J047991.raw

ENTERED

3 <110> APPLICANT: REED, ROBIN
4 ZHOU, ZHAOLAN
6 <120> TITLE OF INVENTION: PURIFICATION OF FUNCTIONAL RIBONUCLEOPROTEIN COMPLEXES
8 <130> FILE REFERENCE: HMV-080.01
10 <140> CURRENT APPLICATION NUMBER: 10/047,991
11 <141> CURRENT FILING DATE: 2002-01-14
13 <150> PRIOR APPLICATION NUMBER: 60/261,521
14 <151> PRIOR FILING DATE: 2001-01-12
16 <160> NUMBER OF SEQ ID NOS: 12
18 <170> SOFTWARE: PatentIn Ver. 2.1
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21 <211> LENGTH: 393
22 <212> TYPE: DNA
23 <213> ORGANISM: Enterobacteria phage MS2
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26 <221> NAME/KEY: CDS
27 <222> LOCATION: (1)..(390)
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32 1 5 10 15
33 ggc gac gtg act gtc gcc cca agc aac ttc gct aac ggg gtc gct gaa 96
34 Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu 30
35 20 25 30
36 tgg atc agc tct aac tcg cgt tca cag gct tac aaa gta acc tgt agc 144
37 Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser 45
38 35 40 45
39 Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu 192
40 50 55 60
41 gtt cgt cag agc tct gcg cag aat cgc aaa tac acc atc aaa gtc gag 240
42 Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val 80
43 65 70 75 80
44 gtc cct aaa gtg gca acc cag act gtt ggt gta gag ctt cct gta 288
45 Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val 95
46 85 90 95
47 gcc gca tgg cgt tcg tac tta aat atg gaa cta acc att cca att ttc 336
48 Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe 110
49 100 105 110
50 Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu 384
51 115 120 125
52 120 125
53 atc tac taa 393

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63 Ile Tyr
 64 130
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 69 <212> TYPE: PRT
 70 <213> ORGANISM: Enterobacteria phage MS2
 72 <400> SEQUENCE: 2
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 74 1 5 10 15
 76 Gly Asp Val Thr Val Ala Pro Ser Asn Phe Ala Asn Gly Val Ala Glu
 77 20 25 30
 79 Trp Ile Ser Ser Asn Ser Arg Ser Gln Ala Tyr Lys Val Thr Cys Ser
 80 35 40 45
 82 Val Arg Gln Ser Ser Ala Gln Asn Arg Lys Tyr Thr Ile Lys Val Glu
 83 50 55 60
 85 Val Pro Lys Val Ala Thr Gln Thr Val Gly Gly Val Glu Leu Pro Val
 86 65 70 75 80
 88 Ala Ala Trp Arg Ser Tyr Leu Asn Met Glu Leu Thr Ile Pro Ile Phe
 89 85 90 95
 91 Ala Thr Asn Ser Asp Cys Glu Leu Ile Val Lys Ala Met Gln Gly Leu
 92 100 105 110
 94 Leu Lys Asp Gly Asn Pro Ile Pro Ser Ala Ile Ala Ala Asn Ser Gly
 95 115 120 125
 97 Ile Tyr
 98 130
 101 <210> SEQ ID NO: 3
 102 <211> LENGTH: 1380
 103 <212> TYPE: DNA
 104 <213> ORGANISM: Escherichia coli
 106 <400> SEQUENCE: 3
 107 tacgtttcgg tttttaggc cggacaaggc gttcacgccc catccggcat ttcacagcat 60
 108 tacttgta tacgagtctg cgcgctttc agggcttcat cgacagtctg acgaccgctg 120
 109 gcggcggtga tcaccgcagt acgcacggca taccagaaag cggacatctg cggatgttc 180
 110 ggcattgatt caccttctg ggcgtttcc atggttgcgg caatacgtgg atcttcgccc 240
 111 aactttcctt cgtaagactt cagcgctacg gcaccagcg gtttgtcttt attaaccgt 300
 112 tccagacctt catcagtcag cagatagttt tcgagaact ctttcgccag ctcttggttc 360
 113 ggactggcgg cgtaataacc tgcgctcagc acgccaacgca acggtttggg tggttgaccc 420
 114 ttgaaggcgg gcagtagccgt tacaccataa ttcaaccttgc tgggtgtcgat gttggaccat 480
 115 gccccacgggc cggttatggt catcgcttt tcgcctttat taaaggcagc ttctgcgtat 540
 116 gagtaatcgg tgtctgcatt catgtgtttt ttttaatca gtcaccccg gaagggtcaga 600
 117 cccgctttcg cgccacgcgtt atccacgccc acgtctttaa tgctgtactt gccgtttca 660
 118 tacttgcacg cataaccccc gtcagcagca atcagcggcc aggtgaaga cggttcttgc 720
 119 aggttgcacg tcagcgcgtt cttaccttgc gctttcgtt ctttatccag cgccggatc 780
 120 tcttcccagg tttttggcgg gttcggcagc agatcttgc tataaatcag cgataacgc 840
 121 tcaacagcga tcgggtaaac aatcagtttgc cgggtgttac gtacggcatc ccaggtaaac 900
 122 ggatacactg tgccttgcgg cgttttgcgg ggggtgattt cagccaaacag gccagattga 960
 123 gcgttagccac caaagcggtc gtgtgcccag aagataatgt cagggccatc gccagttgcc 1020
 124 gcaacacttgc ggaatttctc ttccagtttgc tccggatgtt cAACGGTGCAC tttaattccg 1080
 125 gatctttctt cgaatttctt accgacttca gcgagaccgt tatagcctt atcggcgtta 1140

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126 atccagatta ccagtttacc ttcttcgatt ttggcgagag ccgaggcgga aaacatcatc 1200
 127 gtcgttaatg cgataatgc gaggatgcgt gcacctgttt ttatttcat aatctatgg 1260
 128 ccttgttggta gaagtgcgt tgaaaacacc taaacgact ctagttctt tatacgc 1320
 129 cctcttcca tcctccttgc ccctacgccc caccgtcgct ttgtgtgatc tctgttacag 1380
 132 <210> SEQ ID NO: 4
 133 <211> LENGTH: 396
 134 <212> TYPE: PRT
 135 <213> ORGANISM: Escherichia coli
 137 <400> SEQUENCE: 4
 138 Met Lys Ile Lys Thr Gly Ala Arg Ile Leu Ala Leu Ser Ala Leu Thr
 139 1 5 10 15
 141 Thr Met Met Phe Ser Ala Ser Ala Leu Ala Lys Ile Glu Glu Gly Lys
 142 20 25 30
 144 Leu Val Ile Trp Ile Asn Gly Asp Lys Gly Tyr Asn Gly Leu Ala Glu
 145 35 40 45
 147 Val Gly Lys Lys Phe Glu Lys Asp Thr Gly Ile Lys Val Thr Val Glu
 148 50 55 60
 150 His Pro Asp Lys Leu Glu Lys Phe Pro Gln Val Ala Ala Thr Gly
 151 65 70 75 80
 153 Asp Gly Pro Asp Ile Ile Phe Trp Ala His Asp Arg Phe Gly Gly Tyr
 154 85 90 95
 156 Ala Gln Ser Gly Leu Leu Ala Glu Ile Thr Pro Asp Lys Ala Phe Gln
 157 100 105 110
 159 Asp Lys Leu Tyr Pro Phe Thr Trp Asp Ala Val Arg Tyr Asn Gly Lys
 160 115 120 125
 162 Leu Ile Ala Tyr Pro Ile Ala Val Glu Ala Leu Ser Leu Ile Tyr Asn
 163 130 135 140
 165 Lys Asp Leu Leu Pro Asn Pro Pro Lys Thr Trp Glu Glu Ile Pro Ala
 166 145 150 155 160
 168 Leu Asp Lys Glu Leu Lys Ala Lys Gly Lys Ser Ala Leu Met Phe Asn
 169 165 170 175
 171 Leu Gln Glu Pro Tyr Phe Thr Trp Pro Leu Ile Ala Ala Asp Gly Gly
 172 180 185 190
 174 Tyr Ala Phe Lys Tyr Glu Asn Gly Lys Tyr Asp Ile Lys Asp Val Gly
 175 195 200 205
 177 Val Asp Asn Ala Gly Ala Lys Ala Gly Leu Thr Phe Leu Val Asp Leu
 178 210 215 220
 180 Ile Lys Asn Lys His Met Asn Ala Asp Thr Asp Tyr Ser Ile Ala Glu
 181 225 230 235 240
 183 Ala Ala Phe Asn Lys Gly Glu Thr Ala Met Thr Ile Asn Gly Pro Trp
 184 245 250 255
 186 Ala Trp Ser Asn Ile Asp Thr Ser Lys Val Asn Tyr Gly Val Thr Val
 187 260 265 270
 189 Leu Pro Thr Phe Lys Gly Gln Pro Ser Lys Pro Phe Val Gly Val Leu
 190 275 280 285
 192 Ser Ala Gly Ile Asn Ala Ala Ser Pro Asn Lys Glu Leu Ala Lys Glu
 193 290 295 300
 195 Phe Leu Glu Asn Tyr Leu Leu Thr Asp Glu Gly Leu Glu Ala Val Asn
 196 305 310 315 320

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198 Lys Asp Lys Pro Leu Gly Ala Val Ala Leu Lys Ser Tyr Glu Glu Glu
199 325 330 335
201 Leu Ala Lys Asp Pro Arg Ile Ala Ala Thr Met Glu Asn Ala Gln Lys
202 340 345 350
204 Gly Glu Ile Met Pro Asn Ile Pro Gln Met Ser Ala Phe Trp Tyr Ala
205 355 360 365
207 Val Arg Thr Ala Val Ile Asn Ala Ala Ser Gly Arg Gln Thr Val Asp
208 370 375 380
210 Glu Ala Leu Lys Asp Ala Gln Thr Arg Ile Thr Lys
211 385 390 395
214 <210> SEQ ID NO: 5
215 <211> LENGTH: 44
216 <212> TYPE: DNA
217 <213> ORGANISM: Artificial Sequence
219 <220> FEATURE:
220 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
222 <400> SEQUENCE: 5
223 caggtcatat gggccgcgg gcttcaact ttactcagtt cgtt 44
226 <210> SEQ ID NO: 6
227 <211> LENGTH: 44
228 <212> TYPE: DNA
229 <213> ORGANISM: Artificial Sequence
231 <220> FEATURE:
232 <223> OTHER INFORMATION: Description of Artificial Sequence: Primer
234 <400> SEQUENCE: 6
235 tgctactcga gggcgcttagc gtatgtccg gagtttgctg cgat 44
238 <210> SEQ ID NO: 7
239 <211> LENGTH: 19
240 <212> TYPE: DNA
241 <213> ORGANISM: Artificial Sequence
243 <220> FEATURE:
244 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
245 recognition oligonucleotide
247 <400> SEQUENCE: 7 19
248 cgtacaccat cagggtacg
251 <210> SEQ ID NO: 8
252 <211> LENGTH: 17
253 <212> TYPE: PRT
254 <213> ORGANISM: Artificial Sequence
256 <220> FEATURE:
257 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
258 fusion peptide
260 <400> SEQUENCE: 8
261 Leu Val Pro Arg Gly Ser His Met Arg Gly Ser His His His His 15
262 1 5 10
264 His
267 <210> SEQ ID NO: 9
268 <211> LENGTH: 7
269 <212> TYPE: PRT

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Output Set: N:\CRF3\05282002\J047991.raw

270 <213> ORGANISM: Artificial Sequence
272 <220> FEATURE:
273 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
274 thrombin cleavage site peptide
276 <400> SEQUENCE: 9
277 Leu Val Pro Arg Gly Ser His
278 1 5
281 <210> SEQ ID NO: 10
282 <211> LENGTH: 10
283 <212> TYPE: PRT
284 <213> ORGANISM: Artificial Sequence
286 <220> FEATURE:
287 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
288 peptide
290 <400> SEQUENCE: 10
291 Met Arg Gly Ser His His His His His His
292 1 5 10
295 <210> SEQ ID NO: 11
296 <211> LENGTH: 455
297 <212> TYPE: DNA
298 <213> ORGANISM: Artificial Sequence
300 <220> FEATURE:
301 <223> OTHER INFORMATION: Description of Artificial Sequence: Synthetic
302 nucleotide sequence
304 <400> SEQUENCE: 11
305 taatacgact cactataggg agaccggcag atcagcttgg ccgcgtccat ctggcatct 60
306 aggatctgat atcatcgatg aattcgagct cggtaccccg ttctgtccca ctctttccg 120
307 catcgctgtc tgcgagggcc agctgttggg gtgagtaactc cctctcaaaa gcgggcatga 180
308 ttctgcctt ctagttatta accctacta aaggcagtag tcaagggtt ctttgaagct 240
309 ttctgtctga ccctgtccct ttttttcca cagctgcagg tcgacgttga ggacaaactc 300
310 ttccggtct ttccagtact cttggatccg atatccgtac accatcaggg tacgagctag 360
311 cccatggcgt acaccatcg ggtacgacta gtatctcg tacaccatca ggtacggaa 420
312 ttctcttagag tcgagttata tagtgtcacc taaat 455
315 <210> SEQ ID NO: 12
316 <211> LENGTH: 6
317 <212> TYPE: PRT
318 <213> ORGANISM: Artificial Sequence
320 <220> FEATURE:
321 <223> OTHER INFORMATION: Description of Artificial Sequence: 6x His tag
323 <400> SEQUENCE: 12
324 His His His His His His
325 1 5

VERIFICATION SUMMARY
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